Biogeography and Phylogeography of Reptiles and Amphibians

Biogeography and Phylogeography

- **Biogeography** is the study of historical processes that affect the geographic distributions of animal and plant species
- **Phylogeography** is the study of historical processes that affect the geographic distribution of genetic variation within species

The difference between biogeography and phylogeography is mostly one of scale

Comoros
Glorioso Islands
Mayotte
Malawi
Mozambique
Juan De Nova Island
Mozambique Channel
Madagascar
Mauritius
Reunion
Swaziland

Biogeography

Global Species Richness

- The global number of species is a balance between two processes
- **Speciation**: the formation of two species from one
- **Extinction**: the death of a species

How fast do new species form?

PNAS

Global patterns of diversification in the history of modern amphibians

Kim Roelants*, David J. Gower†, Mark Wilkinson†, Simon P. Loader†, S. D. Biju*‡, Karen Guillaume*, Linde Moriau*, and Franky Bossuyt*§

*Unit of Ecology and Systematics, Vrije Universiteit Brussel, Pleinlaan 2, B-1050 Brussels, Belgium; †Department of Zoology, Natural History Museum, London SW7 5BD, United Kingdom; and ‡Centre for Environmental Management of Degraded Ecosystems, School of Environmental Studies, University of Delhi, Delhi 110007, India

Edited by Francisco J. Ayala, University of California, Irvine, CA, and approved November 21, 2006 (received for review September 22, 2006)

Roelants et al. 2007 PNAS 104: 887

create phylogenetic tree using 5 genes
(one mtDNA, 4 nDNA)

a
350
300
250
200
150
100
50
0 (Mya)
Dev.
Carboniferous
Permian
Triassic
Jurassic
Early Cret.
Late Cret.
Paleogene
Neogene
Gymnophiona
Caudata
Anura
Neobatrachia
Rhinatrematidae
Ichthyophidae
Caecilidae
Cryptobranchidae
Hynobiidae
Sirenidae
Ambystomatidae
Salamandridae
Proteidae
Rhyacotritonidae
Amphiumidae
Plethodontidae
Leiopelmatidae
Alytidae
Bombinatoridae
Rhinophrynidae
Pipidae
Scaphiopodidae
Pelodytidae
Pelobatidae
Megophryidae
Heleophrynidae
Batrachophrynidae
Limnodynastidae
Myobatrachidae
Cycloramphinae
Ceratophryidae
Hylidae
Brachycephalidae
Phyllomedusinae
Pelodryadinae
Centrolenidae
Leptodactylidae
Alsodinae
Dendrobatidae
Bufonidae
Nobleobatrachia [Hylodes]
Sooglossidae
Nasikabatrachidae
Ranixalinae
Ptychadeniidae
Phrynobatrachidae
Petropedetidae
Pyxicephalidae
Microhylidae
Nyctibatrachidae
Dicroglossidae
Ceratobatrachidae
Ranidae
Rhacophoridae
Mantellidae
Hemisotidae
Brevicipitidae
Hyperoliidae
Arthroleptidae
Natatanura [Ranidae]
Microhylidae

Andrias — Cryptobranchidae

Batrachuperus, *Hynobius* — Hynobiidae

Siren — Sirenidae

Ambystoma, *Dicamptodon* — Ambystomatidae

Salamandra, *Pleurodeles*, *Tylototriton*, *Taricha*, *Calotriton*, *Triturus* — Salamandridae

Proteus, *Necturus* — Proteidae

Rhyacotriton — Rhyacotritonidae

Amphiuma — Amphiumidae

Bolitoglossa, *Eurycea*, *Pseudotriton*, *Plethodon*, *Desmognathus*, *Ensatina*, *Hydromantes*, *Speleomantes* — Plethodontidae

t1
n1
n2
t2

Net diversification rate:

speciation - extinction

Net diversification rates vary tremendously across clades

b
Leiopelmatidae
Gymnophiona
Caudata
Amphibia
Salamandridae
Anura
Neobatrachia
Plethodontidae
Microhylidae
Natatanura
Nobleobatrachia
Clade
60
55
50
45
40
35
30
25
20
15
10
5
1
0
0.02
0.04
0.06
0.08
0.1
0.12
Net diversification rate
(events/ lineage/ Myr)

Species composition differed in the past

Late Cretaceous
(99.6 Mya)
Present
45
6009
11
553
24
5283
Gymnophiona
Caudata
Salamandridae
Plethodontidae
Anura
Natatanura
Microhylidae
Nobleobatrachia

Diversification rates have varied through time

b
Triassic
Jurassic
Cretaceous
Tertiary
0.04
0.035
0.03
0.025
0.02
0.015
0.01
0.005
0
net diversification
280
260
240
220
200
180
160
140
120
100
80
60
40
20
Time (Mya)

Diversification rates have varied through space

Pyron and Wiens 2013

6
Lungfish
Gymnophiona
Anura
Caudata
Mammalia
Sphenodontida
Squamata
Testudines
Crocodilia
Aves

6
200
6449
668
5500
2
9671
341
25
10,000
Lungfish
Gymnophiona
Anura
Caudata
Mammalia
Sphenodontida
Squamata
Testudines
Crocodilia
Aves

6
200
6449
668
5500
2
9671
341
25
10,000
Lungfish
Gymnophiona
Anura
Caudata
Mammalia
Sphenodontida
Squamata
Testudines
Crocodilia
Aves

Comoros
Glorioso Islands
Mayotte
Malawi
Mozambique
Juan De Nova Island
Mozambique Channel
Madagascar
Mauritius
Reunion
Swaziland

Historical Biogeography

- Study of the interaction between geography, ecology, and evolution
- Why are species found in the places where they live?
- Special problems: disjunct distributions, endemic species

225 million years ago
Laurasia
Gondwanaland
135 million years ago
North America
Eurasia
Africa
India
South America
Mada-
gascar
Aust-
ralia
Antarctica
65 million years ago
North America
Eurasia
Africa
South America
Mada-
gascar
Aust-
ralia
Antarctica
Present

Figure 13.6. Biogeographic realms of the world.

Main Biogeographic Explanations

- Vicariance: species ranges are explained by splitting due to the formation of barriers
- Dispersal: species ranges are explained by movements (dispersal) into new areas

T_1

T_2
T_1

T3
T2
T1
1
2
3
4
1
2
3
4

Vicariance
Vicariance with Dispersal
1 1 2 3 3 3 4 4
1 1 2 3 3 3 4 4
T3
T2
T1
2
4
1
3
2
4
1
3
T3
T2
T1

Vicariance Example

Lachesis muta

Zamudio and Greene 1997

Vicariance Example

Dispersal Example

Chamaeleo parsonii

Raxworthy et al. 2002

Dispersal Example

Raxworthy et al. 2002

a
North America
Asia
South America and Africa
Madagascar/India, Antarctica, and Australia
170 Ma
b
North America
Asia
South America and Africa
Madagascar/India, Antarctica, and Australia
162 Ma
c
North America
Asia
South America and Africa
Madagascar/ India
Antarctica
Australia
135 Ma
d
North America
Asia
South America
Africa
Madagascar/ India
Australia
100 Ma
e
North America
Asia
South America
Africa
India
Madagascar
Australia
88 Ma
f
North America
Asia
South America
Africa
India
Madagascar
Australia
60 Ma

Figure 1

Stem divergence times
b
Frequency
Age (Ma)

Notice: timing is key!

Modern Biogeography

- Use phylogeny plus distributional data
- Infer the history of taxa: vicariance, dispersal, both?
- Infer the history of areas: concordant patterns among taxa reflect Earth's history

Comoros
Glorioso Islands
Mayotte
Malawi
Mozambique
Juan De Nova Island
Mozambique Channel
Madagascar
Mauritius
Reunion
Swaziland

Phylogeography

- Sample many individuals within one or a few closely related species
- Cover the species' geographic range
- Sequence DNA
- Analyze spatial patterns of genetic variation within and across species

Phylogeography

- Study migration and gene flow across a landscape
- Investigate population fragmentation and speciation

ECOLOGY LETTERS

Ecology Letters, (2013) **16**: 175–182 doi: 10.1111/ele.12025

LETTER

Quantifying the roles of ecology and geography in spatial genetic divergence

Ian J. Wang,[1]* Richard E. Glor[2] and Jonathan B. Losos[1]

[1]*Department of Organismic and Evolutionary Biology, Harvard University, Cambridge, MA, 02138, USA*

[2]*Department of Biology, University of Rochester, Rochester, NY, 14627, USA*

**Correspondence:*
E-mail: ianwang@fas.harvard.edu

Abstract

Investigating the properties of ecological landscapes that influence gene flow among populations can provide key insights into the earliest stages of biological divergence. Both ecological and geographical factors can reduce gene flow, which can lead to population divergence, but we know little of the relative strengths of these phenomena in nature. Here, we use a novel application of structural equation modelling to quantify the contributions of ecological and geographical isolation to spatial genetic divergence in 17 species of *Anolis* lizards. Our comparative analysis shows that although both processes contributed significantly, geographical isolation explained substantially more genetic divergence than ecological isolation (36.3 vs. 17.9% of variance respectively), suggesting that despite the proposed ubiquity of ecological divergence, non-ecological factors play the dominant role in the evolution of spatial genetic divergence.

Keywords

Biogeography, ecological isolation, gene flow, genetic divergence, isolation by distance, structural equation modelling.

Anolis allisoni

Extensive geographic samples from anoles

17 widespread species across four islands

Variety of gene sequence datasets

Bioclim data

What factors explain levels of genetic divergence within species?

Structured Equation Modeling (SEM)

IBD = isolation by distance

physical distance and barriers reduce gene flow between populations

IBD = isolation by distance

physical distance and barriers reduce gene flow between populations

IBE = isolation by environment

adaptive differences or natural selection against dispersers limit gene flow between divergent habitats

Isolation-by-Environment
Isolation-by-Distance
Cuba
Hispaniola
Jamaica
Puerto Rico
Proportion of genetic divergence
1.00
0.80
0.60
0.40
0.20
0
A. allisoni
A. equestris
A. porcatus
A. sagrei
A. chlorocyanus
A. cybotes
A. d. dominicensis
A. d. ignigularis
A. whitemani
A. garmani
A. grahami
A. lineatopus
A. cooki
A. cristatellus
A. krugi
A. poncensis
A. stratulus

Conclusion: both physical distance and natural selection shape genetic variation within species of *Anolis* lizards

Comoros
Glorioso Islands
Mayotte
Malawi
Mozambique
Juan De Nova Island
Mozambique Channel
Madagascar
Mauritius
Reunion
Swaziland